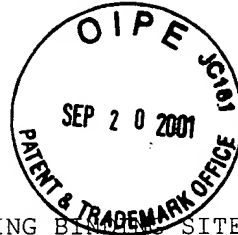


SEQUENCE LISTING

<110> KUFER, Peter
 RAUM, Tobias
 BORSCHERT, Katrin
 ZETTL, Florian
 LUTTERBUSE, Ralf



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 TECH CENTER 1600/2900

<120> A NOVEL METHOD OF IDENTIFYING BINDING SITE DOMAINS THAT RETAIN THE
 CAPACITY OF BINDING TO AN EPITOPE

<130> 0147-0199P

<140> US 09/554,465

<141> 2000-10-19

<160> 77

<170> PatentIn version 3.1

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<220>

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<400> 9
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ccag 64

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<210> 11
<211> 29
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<210> 12
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<220>
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 <220>
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 <210> 14
 <211> 38
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 <400> 14
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 <211> 33
 <212> DNA
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 <220>
 <223> primer for V(L) chain of human anti-17-1A antibody

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 <220>
 <223> oligomer encoding six HIS residues

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 <210> 17
 <211> 24

<212> DNA
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 <220>
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 <210> 18
 <211> 47
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 <220>
 <223> oligonucleotide for multiple cloning site containing SacI and Xho
 I overhang

 <400> 18
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 <210> 19
 <211> 55
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide for multiple cloning site containing SacI and Xho
 I overhang

 <400> 19
 tcgagcagct gcacctcgga tccaccacct cggatttgt cgaccagctg cagct 55

 <210> 20
 <211> 79
 <212> DNA
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 <220>
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 <400> 20
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 ggtggttctg agctcgga 79

 <210> 21
 <211> 79
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide containing multiple cloning sites

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 gaggagacgg tgaccgggc 79

<210> 22
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer for M13 gene III domain N2

<400> 22
 ggtgtcgaca ctaaacctcc tgagtacgg 29

<210> 23
 <211> 30
 <212> DNA
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<220>
 <223> primer for the M13 gene III domain N2

<400> 23
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 <212> DNA
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<220>
 <223> primer for detection of positive clones

<400> 24
 gcagaattca ccatgggcca cacacggagg cag 33

<210> 25
 <211> 39
 <212> DNA
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<220>
 <223> primer for detection of positive clones

<400> 25
 tgggtgacta gtcgtacgtt tgatctcaag cttggtccc 39

<210> 26
 <211> 32

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer for the extracellular region of the human CD54 antigen known as ICAM-1

 <400> 26
 ctccaattca ctatggctcc cagcagcccc cg 32

 <210> 27
 <211> 30
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer for the extracellular region of the human CD54 antigen known as ICAM-1

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 <210> 28
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer for the extracellular region of human CD58

 <400> 28
 aatctagaac catggttgct gggagcgacg 30

 <210> 29
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer for the extracellular region of human CD58

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 aagtccggat ctgtgtcttg aatgaccgct gc 32

 <210> 30
 <211> 32
 <212> DNA
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 <220>
 <223> primer for the extracellular region of human CD86 costimulatory protein

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aagtctagaa aatggatccc cagtgcacta tg 32

<210> 31
<211> 34
<212> DNA
<213> Artificial Sequence

<220>
<223> primer for the extracellular region of human CD86 costimulatory protein

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<210> 32
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<212> DNA
<213> Artificial Sequence

<220>
<223> primers for murine V heavy chain

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saggtgcagc tcgaggagtc aggacct 27

<210> 33
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<220>
<223> primers for murine V heavy chain

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gaggtccagc tcgagcagtc tggacct 27

<210> 34
<211> 27
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<220>
<223> primers for murine V heavy chain

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<220>
 <223> primers for murine V heavy chain

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 <220>
 <223> primers for murine V heavy chain

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 <210> 37
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 <220>
 <223> primers for murine V heavy chain

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 <223> primers for murine V heavy chain

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 <223> primers for murine V heavy chain

 <400> 39
 gaggttcagc tcgagcagtc tggagct 27

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<211> 34
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 <220>
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 <210> 41
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 <212> DNA
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 <220>
 <223> primer for murine V kappa chain

 <400> 41
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 <210> 42
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 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer for murine V kappa chain

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 ccagttccga gctcgtggtg acgcagccgc cc 32

 <210> 43
 <211> 32
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 <223> primer for murine V kappa chain

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 ccagttccga gctcgtgctc acccagtctc ca 32

 <210> 44
 <211> 32
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 <220>
 <223> primer for murine V kappa chain

 <400> 44
 ccagttccga gctccagatg acccagtctc ca 32

<210> 45
 <211> 32
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer for murine V kappa chain

 <400> 45
 ccagatgtga gctcgtgatg acccagactc ca 32

 <210> 46
 <211> 32
 <212> DNA
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 <220>
 <223> primer for murine V kappa chain

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 ccagatgtga gctcgtcatg acccagtctc ca 32

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 <211> 32
 <212> DNA
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 ccagttccga gctcgtgatg acacagtctc ca 32

 <210> 48
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer for murine V kappa chain

 <400> 48
 tgggtgacta gtcgtacgtt tgatctcaag cttggtccc 39

 <210> 49
 <211> 67
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> oligonucleotide for the multiple cloning site

<400> 49
 ctagaattct tcgaatccgg aggtggtgga tccgatatcc ccgggcatca tcaccatcat 60
 cattgag 67

<210> 50
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence of double-stranded oligonucleotide designated ACCGS1BAM

<400> 50
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<210> 51
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence of double-stranded oligonucleotide designated ACCGS15BAM

<400> 51
 gatccaccac cgctgaacc tccacccccg gaaccaccac ct 42

<210> 52
 <211> 14
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> peptide encoded by synthetic oligonucleotide

<400> 52

Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly
 1 5 10

<210> 53
 <211> 381
 <212> DNA
 <213> Homo sapiens

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 <221> CDS
 <222> (1)..(381)
 <223>

<400> 53

gag gtg cag ctg ctc gag tct ggg gga ggc gtg gtc cag cct ggg agg	48
Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg	
1 5 10 15	
tcc ctg aga ctc tcc tgt gca gcc tct gga ttc acc ttc agt agc tat	96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
20 25 30	
ggc atg cac tgg gtc cgc cag gct cca ggc aag ggg ctg gag tgg gtg	144
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
gca gtt ata tca tat gat gga agt aat aaa tac tat gca gac tcc gtg	192
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	
50 55 60	
aag ggc cga ttc acc atc tcc aga gac aat tcc aag aac acg ctg tat	240
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
ctg caa atg aac agc ctg aga gct gag gac acg gct gtg tat tac tgt	288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
gcg aaa gat atg ggg tgg ggc agt ggc tgg aga ccc tac tac tac tac	336
Ala Lys Asp Met Gly Trp Gly Ser Gly Trp Arg Pro Tyr Tyr Tyr Tyr	
100 105 110	
ggt atg gac gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tca	381
Gly Met Asp Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser	
115 120 125	

<210> 54
 <211> 127
 <212> PRT
 <213> Homo sapiens

<400> 54

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
20 25 30	
Gly Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ala Val Ile Ser Tyr Asp Gly Ser Asn Lys Tyr Tyr Ala Asp Ser Val	
50 55 60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	

65		70		75		80									
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
			85						90					95	
Ala	Lys	Asp	Met	Gly	Trp	Gly	Ser	Gly	Trp	Arg	Pro	Tyr	Tyr	Tyr	Tyr
			100					105					110		
Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	
		115					120					125			

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 <213> Homo sapiens

<220>
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 <222> (1)..(321)
 <223>

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Glu	Leu	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	
1				5					10					15		
gac	aga	gtc	acc	atc	act	tgt	cgg	aca	agt	cag	agc	att	agc	agc	tat	96
Asp	Arg	Val	Thr	Ile	Thr	Cys	Arg	Thr	Ser	Gln	Ser	Ile	Ser	Ser	Tyr	
			20					25					30			
tta	aat	tgg	tat	cag	cag	aaa	cca	gga	cag	cct	cct	aag	ctg	ctc	att	144
Leu	Asn	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	
		35					40					45				
tac	tgg	gca	tct	acc	cgg	gaa	tcc	ggg	gtc	cct	gac	cga	ttc	agt	ggc	192
Tyr	Trp	Ala	Ser	Thr	Arg	Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	
	50					55				60						
agc	ggg	tct	ggg	aca	gat	ttc	act	ctc	acc	atc	agc	agt	cta	caa	cct	240
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	
65				70					75					80		
gaa	gat	tct	gca	act	tac	tac	tgt	cag	cag	agt	tac	gac	atc	cgc	tac	288
Glu	Asp	Ser	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Ser	Tyr	Asp	Ile	Pro	Tyr	
			85					90					95			
act	ttt	ggc	cag	ggg	acc	aag	ctg	gag	atc	aaa						321
Thr	Phe	Gly	Gln	Gly	Thr	Lys	Leu	Glu	Ile	Lys						
			100					105								

<210> 56

<211> 107
 <212> PRT
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<400> 56

Glu Leu Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Thr Ser Gln Ser Ile Ser Ser Tyr
 20 25 30

Leu Asn Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile
 35 40 45

Tyr Trp Ala Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Ser Gly
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65 70 75 80

Glu Asp Ser Ala Thr Tyr Tyr Cys Gln Gln Ser Tyr Asp Ile Pro Tyr
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Leu Glu Ile Lys
 100 105

<210> 57
 <211> 201
 <212> DNA
 <213> Artificial Sequence

<220>

<223> sequence designated L-F-NS3Frame (Figure 3.4)

<400> 57
 ccgctctaga attccaccat gggatggagc tgtatcatcc tcttcttggt agcaacagct 60
 acaggtgtcc actccgacta caaagatgat gacgataagg atatcttcgg aggtggtggt 120
 agcgctattc catatggacg tcccgctcga ggctcgtocat catcaccatc atcactgagc 180
 ggccgctcta gactcgacct c 201

<210> 58
 <211> 526
 <212> DNA
 <213> Artificial Sequence

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<220>
<223> M13-Phage and artificial sequence of the MCS

<220>
<221> CDS
<222> (19)..(429)
<223>

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                1          5          10

ccg ggc tat act tat atc aac cct ctc gac ggc act tat ccg cct ggt      99
Pro Gly Tyr Thr Tyr Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly
                15          20          25

act gag caa aac ccc gct aat cct aat cct tct ctt gag gag tct cag      147
Thr Glu Gln Asn Pro Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln
                30          35          40

cct ctt aat act ttc atg ttt cag aat aat agg ttc cga aat agg cag      195
Pro Leu Asn Thr Phe Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln
                45          50          55

ggg gca tta act gtt tat acg ggc act gtt act caa ggc act gac ccc      243
Gly Ala Leu Thr Val Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro
                60          65          70          75

gtt aaa act tat tac cag tac act cct gta tca tca aaa gcc atg tat      291
Val Lys Thr Tyr Tyr Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr
                80          85          90

gac gct tac tgg aac ggt aaa ttc aga gac tgc gct ttc cat tct ggc      339
Asp Ala Tyr Trp Asn Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly
                95          100          105

ttt aat gag gat cca ttc gtt tgt gaa tat caa ggc caa tcg tct gac      387
Phe Asn Glu Asp Pro Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp
                110          115          120

ctg cct caa cct cct gtc aat gct tcc gga ggt ggt gga tcc      429
Leu Pro Gln Pro Pro Val Asn Ala Ser Gly Gly Gly Gly Ser
                125          130          135

gaggtgcagc tgctcgagcc cggtcaccgt ctctcaggt ggtggtggtt ctggcggcgg      489

cggctccggt ggtggtggtt ctgagctcgg gactagt      526

<210> 59
<211> 137
<212> PRT
<213> Artificial Sequence

<220>

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<223> M13-Phage and artificial sequence of the MCS

<400> 59

Thr Lys Pro Pro Glu Tyr Gly Asp Thr Pro Ile Pro Gly Tyr Thr Tyr
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Ile Asn Pro Leu Asp Gly Thr Tyr Pro Pro Gly Thr Glu Gln Asn Pro
20 25 30

Ala Asn Pro Asn Pro Ser Leu Glu Glu Ser Gln Pro Leu Asn Thr Phe
35 40 45

Met Phe Gln Asn Asn Arg Phe Arg Asn Arg Gln Gly Ala Leu Thr Val
50 55 60

Tyr Thr Gly Thr Val Thr Gln Gly Thr Asp Pro Val Lys Thr Tyr Tyr
65 70 75 80

Gln Tyr Thr Pro Val Ser Ser Lys Ala Met Tyr Asp Ala Tyr Trp Asn
85 90 95

Gly Lys Phe Arg Asp Cys Ala Phe His Ser Gly Phe Asn Glu Asp Pro
100 105 110

Phe Val Cys Glu Tyr Gln Gly Gln Ser Ser Asp Leu Pro Gln Pro Pro
115 120 125

Val Asn Ala Ser Gly Gly Gly Gly Ser
130 135

<210> 60
<211> 726
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(726)
<223>

<400> 60
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Glu Val Gln Leu Glu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly
1 5 10 15

gcc tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc act aac 96

Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ala	Phe	Thr	Asn		
			20					25					30				
tac	tgg	cta	ggg	tgg	gta	aag	cag	agg	cct	gga	cat	gga	ctt	gag	tgg	144	
Tyr	Trp	Leu	Gly	Trp	Val	Lys	Gln	Arg	Pro	Gly	His	Gly	Leu	Glu	Trp		
		35				40					45						
att	gga	gat	ctt	ttc	cct	gga	agt	ggg	aat	act	cac	tac	aat	gag	agg	192	
Ile	Gly	Asp	Leu	Phe	Pro	Gly	Ser	Gly	Asn	Thr	His	Tyr	Asn	Glu	Arg		
	50					55				60							
ttc	agg	ggc	aaa	gcc	aca	ctg	act	gca	gac	aaa	tcc	tcg	agc	aca	gcc	240	
Phe	Arg	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala		
65					70					75					80		
ttt	atg	cag	ctc	agt	agc	ctg	aca	tct	gag	gac	tct	gct	gtc	tat	ttc	288	
Phe	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe		
				85					90				95				
tgt	gca	aga	ttg	agg	aac	tgg	gac	gag	gct	atg	gac	tac	tgg	ggc	caa	336	
Cys	Ala	Arg	Leu	Arg	Asn	Trp	Asp	Glu	Ala	Met	Asp	Tyr	Trp	Gly	Gln		
			100					105					110				
ggg	acc	acg	gtc	acc	gtc	tcc	tca	ggg	ggg	ggg	ggg	tct	ggc	ggc	ggc	384	
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly		
		115				120						125					
ggc	tcc	ggg	ggg	ggg	ggg	tct	gag	ctc	gtc	atg	acc	cag	tct	cca	tct	432	
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu	Val	Met	Thr	Gln	Ser	Pro	Ser		
	130					135					140						
tat	ctt	gct	gca	tct	cct	gga	gaa	acc	att	act	att	aat	tgc	agg	gca	480	
Tyr	Leu	Ala	Ala	Ser	Pro	Gly	Glu	Thr	Ile	Thr	Ile	Asn	Cys	Arg	Ala		
145					150					155					160		
agt	aag	agc	att	agc	aaa	tat	tta	gcc	tgg	tat	caa	gag	aaa	cct	ggg	528	
Ser	Lys	Ser	Ile	Ser	Lys	Tyr	Leu	Ala	Trp	Tyr	Gln	Glu	Lys	Pro	Gly		
				165					170					175			
aaa	act	aat	aag	ctt	ctt	atc	tac	tct	gga	tcc	act	ttg	caa	tct	gga	576	
Lys	Thr	Asn	Lys	Leu	Leu	Ile	Tyr	Ser	Gly	Ser	Thr	Leu	Gln	Ser	Gly		
			180					185					190				
att	cca	tca	agg	ttc	agt	ggc	agt	gga	tct	ggg	aca	gat	ttc	act	ctc	624	
Ile	Pro	Ser	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu		
		195				200						205					
acc	atc	agt	agc	ctg	gag	cct	gaa	gat	ttt	gca	atg	tat	tac	tgt	caa	672	
Thr	Ile	Ser	Ser	Leu	Glu	Pro	Glu	Asp	Phe	Ala	Met	Tyr	Tyr	Cys	Gln		
	210					215				220							
cag	cat	aat	gaa	tat	ccg	tac	acg	ttc	gga	ggg	ggg	acc	aag	ctt	gag	720	
Gln	His	Asn	Glu	Tyr	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu		
225					230					235					240		
atc	aaa															726	
Ile	Lys																

<210> 61
 <211> 242
 <212> PRT
 <213> Mus sp.

<400> 61

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Lys Pro Gly
 1 5 10 15

Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Ile Gly Asp Leu Phe Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
 50 55 60

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
 145 150 155 160

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly
 165 170 175

Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly
 180 185 190

Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 195 200 205

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln
 210 215 220

Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
 225 230 235 240

Ile Lys

<210> 62
 <211> 753
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(753)
 <223>

<400> 62
 gag gtg cag ctg ctc gag cag tct gga gct gag ctg gta agg cct ggg 48
 Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15
 act tca gtg aag ctg tcc tgc aag gct tct ggc tac acc ttc aca agc 96
 Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
 20 25 30
 tat ggt tta agc tgg gtg aag cag aga act gga cag ggc ctt gag tgg 144
 Tyr Gly Leu Ser Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp
 35 40 45
 att gga gag gtt tat cct aga att ggt aat gct tac tac aat gag aag 192
 Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys
 50 55 60
 ttc aag ggc aag gcc aca ctg act gca gac aaa tcc tcc agc aca gcg 240
 Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80
 tcc atg gag ctc cgc agc ctg aca tct gag gac tct gcg gtc tat ttc 288
 Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
 85 90 95
 tgt gca aga cgg gga tcc tac ggt agt aac tac gac tgg tac ttc gat 336
 Cys Ala Arg Arg Gly Ser Tyr Gly Ser Asn Tyr Asp Trp Tyr Phe Asp
 100 105 110

gtc tgg ggc caa ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt	384
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly	
115 120 125	
tct ggc ggc ggc ggc tcc ggt ggt ggt ggt tct gag ctc gtg atg acc	432
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr	
130 135 140	
cag act cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc	480
Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile	
145 150 155 160	
tct tgc aga tct agt cag agc ctt gta cac agt aat gga aac acc tat	528
Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr	
165 170 175	
tta cat tgg tac ctg cag aag cca ggc cag tct cca aag ctc ctg atc	576
Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile	
180 185 190	
tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc	624
Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly	
195 200 205	
agt gga tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct	672
Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala	
210 215 220	
gag gat ctg gga gtt tat ttc tgc tct caa agt aca cat gtt ccg tac	720
Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr	
225 230 235 240	
acg ttc gga ggg ggg acc aag ctt gag atc aaa	753
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
245 250	

<210> 63
 <211> 251
 <212> PRT
 <213> Mus sp.

<400> 63

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Ser
20 25 30

Tyr Gly Leu Ser Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp
35 40 45

Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys

50		55		60
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala				
65		70		75 80
Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe				
	85		90	95
Cys Ala Arg Arg Gly Ser Tyr Gly Ser Asn Tyr Asp Trp Tyr Phe Asp				
	100		105	110
Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly				
	115		120	125
Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr				
	130		135	140
Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile				
145		150		155 160
Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr				
	165		170	175
Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile				
	180		185	190
Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly				
	195		200	205
Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala				
	210		215	220
Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr				
225		230		235 240
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys				
	245		250	

<210> 64
 <211> 726
 <212> DNA
 <213> Mus sp.

<220>

<221> CDS
 <222> (1)..(726)
 <223>

<400> 64

gag gtg cag ctg ctc gag cag tct gga gct gcg ctg gta agg cct ggg	48
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Ala Leu Val Arg Pro Gly	
1 5 10 15	
act tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc act aac	96
Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn	
20 25 30	
tac tgg cta ggt tgg gta aag cag agg cct gga cat gga ctt gag tgg	144
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp	
35 40 45	
att gga gat att tac cct gga agt ggt aat act cac tac aat gag agg	192
Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg	
50 55 60	
ttc agg ggc aaa gcc aca ctg act gca gac aaa tcc tcg agc aca gcc	240
Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala	
65 70 75 80	
ttt atg cag ctc agt agc ctg aca tct gag gac tct gct gtc tat ttc	288
Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe	
85 90 95	
tgt gca aga ttg agg aac tgg gac gag cct atg gac tac tgg ggc caa	336
Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln	
100 105 110	
ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt tct ggc ggc ggc	384
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly	
115 120 125	
ggc tcc ggt ggt ggt ggt tct gag ctc cag atg acc cag tct cca tct	432
Gly Ser Gly Gly Gly Gly Ser Glu Leu Gln Met Thr Gln Ser Pro Ser	
130 135 140	
tat ctt gct gca tct cct gga gaa acc att act att aat tgc agg gca	480
Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala	
145 150 155 160	
agt aag agc att agc aaa tat tta gcc tgg tat caa gag aaa cct ggg	528
Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly	
165 170 175	
aaa act aat aag ctt ctt atc tac tct gga tcc act ttg caa tct gga	576
Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly	
180 185 190	
att cca tca agg ttc agt ggc agt gga tct ggt aca gat ttc act ctc	624
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu	
195 200 205	

acc atc agt agc ctg gag cct gaa gat ttt gca atg tat tac tgt caa	672
Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln	
210 215 220	

cag cat aat gaa tac ccg tac acg ttc gga ggg ggg acc aag ctt gag	720
Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu	
225 230 235 240	

atc aaa	726
Ile Lys	

<210> 65
 <211> 242
 <212> PRT
 <213> Mus sp.

<400> 65

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Ala Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
50 55 60

Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80

Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Gln Met Thr Gln Ser Pro Ser
130 135 140

Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
 145 150 155 160

Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly
 165 170 175

Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly
 180 185 190

Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 195 200 205

Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln
 210 215 220

Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
 225 230 235 240

Ile Lys

<210> 66
 <211> 744
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(744)
 <223>

<400> 66
 gag gtg cag ctg ctc gag cag tct gga gct gag ctg gta agg cct ggg 48
 Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15
 act tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc act aac 96
 Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30
 tac tgg cta ggt tgg gtt aag cag agg cct gga cat gga ctt gaa tgg 144
 Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45
 gtt gga gat att ttc cct gga agt ggt aat gct cac tac aat gag aag 192
 Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys
 50 55 60
 ttc aag ggc aaa gcc aca ctg act gca gac aag tcc tcg tac aca gcc 240

Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Tyr	Thr	Ala		
65					70					75					80		
tat	atg	cag	ctc	agt	agc	ctg	aca	tct	gag	gac	tct	gct	gtc	tat	ttc		288
Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe		
				85					90					95			
tgt	gca	aga	ttg	cgg	aac	tgg	gac	gag	gct	atg	gac	tac	tgg	ggc	caa		336
Cys	Ala	Arg	Leu	Arg	Asn	Trp	Asp	Glu	Ala	Met	Asp	Tyr	Trp	Gly	Gln		
			100					105					110				
ggg	acc	acg	gtc	acc	gtc	tcc	tca	ggg	ggg	ggg	ggg	tct	ggc	ggc	ggc		384
Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly		
			115					120					125				
ggc	tcc	ggg	ggg	ggg	ggg	tct	gag	ctc	gtg	atg	aca	cag	tct	cca	tcc		432
Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu	Val	Met	Thr	Gln	Ser	Pro	Ser		
	130					135					140						
tcc	ctg	agt	gtg	tca	gca	gga	gag	aag	gtc	act	atg	agc	tgc	aag	tcc		480
Ser	Leu	Ser	Val	Ser	Ala	Gly	Glu	Lys	Val	Thr	Met	Ser	Cys	Lys	Ser		
145					150					155					160		
agt	cag	agt	ctg	tta	aac	agt	gga	aat	caa	aag	aac	tac	ttg	gcc	tgg		528
Ser	Gln	Ser	Leu	Leu	Asn	Ser	Gly	Asn	Gln	Lys	Asn	Tyr	Leu	Ala	Trp		
				165					170					175			
tac	cag	cag	aaa	cca	ggg	cag	cct	cct	aaa	ctg	ttg	atc	tac	ggg	gca		576
Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Pro	Pro	Lys	Leu	Leu	Ile	Tyr	Gly	Ala		
			180						185					190			
tcc	act	agg	gaa	tct	ggg	gtc	cct	gat	cgc	ttc	aca	ggc	agt	gga	tct		624
Ser	Thr	Arg	Glu	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser		
			195				200					205					
gga	aca	gat	ttc	act	ctc	acc	atc	agc	agt	gtg	cag	gct	gaa	gac	ctg		672
Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Val	Gln	Ala	Glu	Asp	Leu		
	210					215					220						
gca	gtt	tat	tac	tgt	cag	aat	gat	tat	agt	tat	ccg	tac	acg	ttc	gga		720
Ala	Val	Tyr	Tyr	Cys	Gln	Asn	Asp	Tyr	Ser	Tyr	Pro	Tyr	Thr	Phe	Gly		
225					230					235					240		
ggg	ggg	acc	aag	ctt	gag	atc	aaa										744
Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys										
				245													

<210> 67
 <211> 248
 <212> PRT
 <213> Mus sp.

<400> 67

Glu	Val	Gln	Leu	Leu	Glu	Gln	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	
1				5					10					15		

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Ser Val Ser Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp
165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala
180 185 190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Tyr Thr Phe Gly
225 230 235 240

Gly Gly Thr Lys Leu Glu Ile Lys
245

<210> 68
<211> 726
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(726)
<223>

<400> 68
gag gtg cag ctg ctc gag cag tct gga gct gag ctg gtg agg cct ggg 48
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15
gct tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc aat aac 96
Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Asn Asn
20 25 30
tac tgg cta ggt tgg gta aag cag agg cct gga cat gga ctt gag tgg 144
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45
att gga gac att tac cct gga agt gga aat act cac tac aat gag agg 192
Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg
50 55 60
ttc agg ggc aaa gcc aca ctg act gca gac aaa tcc tcg agc aca gcc 240
Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
65 70 75 80
ttt atg cag tta agt agc ctg aca tct gag gac tct gct gtc tat ttc 288
Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95
tgt gca aga ttg agg aac tgg gac gag gct atg gac tac tgg ggc caa 336
Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110
ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt tct ggc ggc ggc 384
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125
ggc tcc ggt ggt ggt ggt tct gag ctc gtc atg acc cag tct cca tct 432
Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140
tat ctt gct gca tct cct gga gaa acc att act att aat tgc agg gca 480
Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
145 150 155 160

agc aag agc att agc aaa tat tta gcc tgg tat caa gag aaa cct ggg	528
Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly	
165 170 175	
aaa act aat aag ctt ctt atc tac tct gga tcc act ttg caa tct gga	576
Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly	
180 185 190	
att cca tca agg ttc agt ggc agt gga tct ggt aca gat ttc act ctc	624
Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu	
195 200 205	
acc atc agt agc ctg gag cct gaa gat ttt gca atg tat tac tgt caa	672
Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln	
210 215 220	
cag cat aat gaa tac ccg tac acg ttc gga ggg ggg acc aag ctt gag	720
Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu	
225 230 235 240	
atc aaa	726
Ile Lys	

<210> 69
 <211> 242
 <212> PRT
 <213> Mus sp.

<400> 69

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly	
1 5 10 15	
Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Asn Asn	
20 25 30	
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp	
35 40 45	
Ile Gly Asp Ile Tyr Pro Gly Ser Gly Asn Thr His Tyr Asn Glu Arg	
50 55 60	
Phe Arg Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala	
65 70 75 80	
Phe Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe	
85 90 95	
Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln	

100 105 110
 Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125
 Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140
 Tyr Leu Ala Ala Ser Pro Gly Glu Thr Ile Thr Ile Asn Cys Arg Ala
 145 150 155 160
 Ser Lys Ser Ile Ser Lys Tyr Leu Ala Trp Tyr Gln Glu Lys Pro Gly
 165 170 175
 Lys Thr Asn Lys Leu Leu Ile Tyr Ser Gly Ser Thr Leu Gln Ser Gly
 180 185 190
 Ile Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 195 200 205
 Thr Ile Ser Ser Leu Glu Pro Glu Asp Phe Ala Met Tyr Tyr Cys Gln
 210 215 220
 Gln His Asn Glu Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
 225 230 235 240

Ile Lys

<210> 70
 <211> 753
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(753)
 <223>

<400> 70
 gag gtg cag ctg ctc gag cag tct gga gct gag ctg gcg agg cct ggg 48
 Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly
 1 5 10 15
 gct tca gtg aag ctg tcc tgc aag gct tct ggc tac acc ttc aca aac 96
 Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn

20				25				30								
tat	ggt	tta	agc	tgg	gtg	aag	cag	agg	cct	gga	cag	gtc	ctt	gag	tgg	144
Tyr	Gly	Leu	Ser	Trp	Val	Lys	Gln	Arg	Pro	Gly	Gln	Val	Leu	Glu	Trp	
35				40				45								
att	gga	gag	gtt	tat	cct	aga	att	ggt	aat	gct	tac	tac	aat	gag	aag	192
Ile	Gly	Glu	Val	Tyr	Pro	Arg	Ile	Gly	Asn	Ala	Tyr	Tyr	Asn	Glu	Lys	
50				55				60								
ttc	aag	ggc	aag	gcc	aca	ctg	act	gca	gac	aaa	tcc	tcc	agc	aca	gcg	240
Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser	Thr	Ala	
65				70				75				80				
tcc	atg	gag	ctc	cgc	agc	ctg	acc	tct	gag	gac	tct	gcg	gtc	tat	ttc	288
Ser	Met	Glu	Leu	Arg	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val	Tyr	Phe	
85				90				95								
tgt	gca	aga	cgg	gga	tcc	tac	gat	act	aac	tac	gac	tgg	tac	ttc	gat	336
Cys	Ala	Arg	Arg	Gly	Ser	Tyr	Asp	Thr	Asn	Tyr	Asp	Trp	Tyr	Phe	Asp	
100				105				110								
gtc	tgg	ggc	caa	ggg	acc	acg	gtc	acc	gtc	tcc	tca	ggt	ggt	ggt	ggt	384
Val	Trp	Gly	Gln	Gly	Thr	Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	
115				120				125								
tct	ggc	ggc	ggc	ggc	tcc	ggg	ggg	ggg	ggg	tct	gag	ctc	gtg	atg	acc	432
Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Glu	Leu	Val	Met	Thr	
130				135				140								
cag	act	cca	ctc	tcc	ctg	cct	gtc	agt	ctt	gga	gat	caa	gcc	tcc	atc	480
Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	
145				150				155				160				
tct	tgc	aga	tct	agt	cag	agc	ctt	gta	cac	agt	aat	gga	aac	acc	tat	528
Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Ser	Asn	Gly	Asn	Thr	Tyr	
165				170				175								
tta	cat	tgg	tac	ctg	cag	aag	cca	ggc	cag	tct	cca	aag	ctc	ctg	atc	576
Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	
180				185				190								
tac	aaa	gtt	tcc	aac	cga	ttt	tct	ggg	gtc	cca	gac	agg	ttc	agt	ggc	624
Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	
195				200				205								
agt	gga	tca	ggg	aca	gat	ttc	aca	ctc	aag	atc	agc	aga	gtg	gag	gct	672
Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Lys	Ile	Ser	Arg	Val	Glu	Ala	
210				215				220								
gag	gat	ctg	gga	gtt	tat	ttc	tgc	tct	caa	agt	aca	cat	gtt	ccg	tac	720
Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	
225				230				235				240				
acg	ttc	gga	ggg	ggg	acc	aag	ctt	gag	atc	aaa						753
Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Glu	Ile	Lys						
245				250												

<210> 71
 <211> 251
 <212> PRT
 <213> Mus sp.

<400> 71

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Ala Arg Pro Gly
 1 5 10 15

Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asn
 20 25 30

Tyr Gly Leu Ser Trp Val Lys Gln Arg Pro Gly Gln Val Leu Glu Trp
 35 40 45

Ile Gly Glu Val Tyr Pro Arg Ile Gly Asn Ala Tyr Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Ser Met Glu Leu Arg Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Arg Gly Ser Tyr Asp Thr Asn Tyr Asp Trp Tyr Phe Asp
 100 105 110

Val Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly
 115 120 125

Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr
 130 135 140

Gln Thr Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile
 145 150 155 160

Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Asn Thr Tyr
 165 170 175

Leu His Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile
 180 185 190

Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly
 195 200 205

Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala
 210 215 220

Glu Asp Leu Gly Val Tyr Phe Cys Ser Gln Ser Thr His Val Pro Tyr
 225 230 235 240

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
 245 250

<210> 72
 <211> 717
 <212> DNA
 <213> Mus sp.

<220>
 <221> CDS
 <222> (1)..(717)
 <223>

<400> 72
 gag gtg cag ctg ctc gag tct gga ggt ggc ctg gtg cag cct gga gga 48
 Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1 5 10 15
 tcc ctg aaa ctc tcc tgt gca gcc tca gga ttc gat ttt agt aga tac 96
 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Asp Phe Ser Arg Tyr
 20 25 30
 tgg atg agt tgg gtc cgg cag gct cca ggg aaa ggg cta gaa tgg att 144
 Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Ile
 35 40 45
 gga gaa att aat cca gat agc agt acg ata aac tat acg cca tct ctg 192
 Gly Glu Ile Asn Pro Asp Ser Ser Thr Ile Asn Tyr Thr Pro Ser Leu
 50 55 60
 aag gat aaa ttc atc atc tcc aga gac aac gcc aaa aat acg ctg tac 240
 Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
 65 70 75 80
 ctg caa atg ggc aaa gtg aga tct gag gac aca gcc ctt tat tac tgt 288
 Leu Gln Met Gly Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
 85 90 95
 gca aga gga gcc ttc ctt ttt gac tac tgg ggc caa ggg acc acg gtc 336
 Ala Arg Gly Ala Phe Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
 100 105 110
 acc gtc tcc tca ggt ggt ggt ggt tct ggc ggc ggc ggc tcc ggt ggt 384

Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly		
		115					120					125					
ggt	ggt	tct	gag	ctc	gtg	ctc	acc	cag	tct	cca	acc	acc	atg	gct	gca	432	
Gly	Gly	Ser	Glu	Leu	Val	Leu	Thr	Gln	Ser	Pro	Thr	Thr	Met	Ala	Ala		
		130				135					140						
tct	ccc	ggg	gag	aag	atc	act	atc	acc	tgc	agt	gcc	agc	tca	agt	ata	480	
Ser	Pro	Gly	Glu	Lys	Ile	Thr	Ile	Thr	Cys	Ser	Ala	Ser	Ser	Ser	Ile		
		145			150					155					160		
agt	tcc	aat	tac	ttg	cat	tgg	tat	cag	cag	aag	cca	gga	ttc	tcc	cct	528	
Ser	Ser	Asn	Tyr	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Phe	Ser	Pro		
				165				170						175			
aaa	ctc	ttg	att	tat	agg	aca	tcc	aat	ctg	gct	tct	gga	gtc	cca	gct	576	
Lys	Leu	Leu	Ile	Tyr	Arg	Thr	Ser	Asn	Leu	Ala	Ser	Gly	Val	Pro	Ala		
			180					185					190				
cgc	ttc	agt	ggc	agt	ggg	tct	ggg	acc	tct	tac	tct	ctc	aca	att	ggc	624	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Gly		
		195				200						205					
acc	atg	gag	gct	gaa	gat	gtt	gcc	act	tac	tac	tgc	cag	cag	ggt	agt	672	
Thr	Met	Glu	Ala	Glu	Asp	Val	Ala	Thr	Tyr	Tyr	Cys	Gln	Gln	Gly	Ser		
		210				215					220						
agt	ata	cca	ctc	acg	ttc	ggt	gct	ggg	acc	aag	ctt	gag	atc	aaa		717	
Ser	Ile	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Ile	Lys			
		225			230					235							

<210> 73
 <211> 239
 <212> PRT
 <213> Mus sp.

<400> 73

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly		
1				5					10					15			
Ser	Leu	Lys	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Asp	Phe	Ser	Arg	Tyr		
			20					25					30				
Trp	Met	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Ile		
		35				40						45					
Gly	Glu	Ile	Asn	Pro	Asp	Ser	Ser	Thr	Ile	Asn	Tyr	Thr	Pro	Ser	Leu		
		50				55					60						
Lys	Asp	Lys	Phe	Ile	Ile	Ser	Arg	Asp	Asn	Ala	Lys	Asn	Thr	Leu	Tyr		
		65			70					75					80		

Leu Gln Met Gly Lys Val Arg Ser Glu Asp Thr Ala Leu Tyr Tyr Cys
85 90 95

Ala Arg Gly Ala Phe Leu Phe Asp Tyr Trp Gly Gln Gly Thr Thr Val
100 105 110

Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125

Gly Gly Ser Glu Leu Val Leu Thr Gln Ser Pro Thr Thr Met Ala Ala
130 135 140

Ser Pro Gly Glu Lys Ile Thr Ile Thr Cys Ser Ala Ser Ser Ser Ile
145 150 155 160

Ser Ser Asn Tyr Leu His Trp Tyr Gln Gln Lys Pro Gly Phe Ser Pro
165 170 175

Lys Leu Leu Ile Tyr Arg Thr Ser Asn Leu Ala Ser Gly Val Pro Ala
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Gly
195 200 205

Thr Met Glu Ala Glu Asp Val Ala Thr Tyr Tyr Cys Gln Gln Gly Ser
210 215 220

Ser Ile Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Ile Lys
225 230 235

<210> 74
<211> 744
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(744)
<223>

<400> 74

gag gtg cag ctg ctc gag cag tct gga gct gag ctg gta agg cct ggg
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

48

act tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc act aac	96
Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn	
20 25 30	
tac tgg cta ggt tgg gta aag cag agg cct gga cat gga ctt gag tgg	144
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp	
35 40 45	
att gga gat att ttc cct gga agt ggt aat atc cac tac aat gag aag	192
Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys	
50 55 60	
ttc aag ggc aaa gcc aca ctg act gca gac aaa tct tcg agc aca gcc	240
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala	
65 70 75 80	
tat atg cag ctc agt agc ctg aca ttt gag gac tct gct gtc tat ttc	288
Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe	
85 90 95	
tgt gca aga ctg agg aac tgg gac gag cct atg gac tac tgg ggc caa	336
Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln	
100 105 110	
ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt tct ggc ggc ggc	384
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly	
115 120 125	
ggc tcc ggt ggt ggt ggt tct gag ctc gtg atg aca cag tct cca tcc	432
Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser	
130 135 140	
tcc ctg act gtg aca gca gga gag aag gtc act atg agc tgc aag tcc	480
Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser	
145 150 155 160	
agt cag agt ctg tta aac agt gga aat caa aag aac tac ttg acc tgg	528
Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp	
165 170 175	
tac cag cag aaa cca ggg cag cct cct aaa ctg ttg atc tac tgg gca	576
Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala	
180 185 190	
tcc act agg gaa tct ggg gtc cct gat cgc ttc aca ggc agt gga tct	624
Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser	
195 200 205	
gga aca gat ttc act ctc acc atc agc agt gtg cag gct gaa gac ctg	672
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu	
210 215 220	
gca gtt tat tac tgt cag aat gat tat agt tat ccg ctc acg ttc ggt	720
Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly	
225 230 235 240	

gct ggg acc aag ctt gag atc aaa
 Ala Gly Thr Lys Leu Glu Ile Lys
 245

744

<210> 75
 <211> 248
 <212> PRT
 <213> Mus sp.

<400> 75

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
 1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
 20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
 35 40 45

Ile Gly Asp Ile Phe Pro Gly Ser Gly Asn Ile His Tyr Asn Glu Lys
 50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
 65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Phe Glu Asp Ser Ala Val Tyr Phe
 85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Pro Met Asp Tyr Trp Gly Gln
 100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
 115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
 130 135 140

Ser Leu Thr Val Thr Ala Gly Glu Lys Val Thr Met Ser Cys Lys Ser
 145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Gly Asn Gln Lys Asn Tyr Leu Thr Trp
 165 170 175

Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu Ile Tyr Trp Ala

180

185

190

Ser Thr Arg Glu Ser Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Asn Asp Tyr Ser Tyr Pro Leu Thr Phe Gly
225 230 235 240

Ala Gly Thr Lys Leu Glu Ile Lys
245

<210> 76
<211> 744
<212> DNA
<213> Mus sp.

<220>
<221> CDS
<222> (1)..(744)
<223>

<400> 76
gag gtg cag ctg ctc gag cag tct gga gct gag ctg gta agg cct ggg 48
Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15
act tca gtg aag ata tcc tgc aag gct tct gga tac gcc ttc act aac 96
Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30
tac tgg cta ggt tgg gtt aag cag agg cct gga cat gga ctt gaa tgg 144
Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45
gtt gga gat att ttc cct gga agt ggt aat gct cac tac aat gag aag 192
Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys
50 55 60
ttc aag ggc aaa gcc aca ctg act gca gac aag tcc tcg tac aca gcc 240
Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala
65 70 75 80
tat atg cag ctc agt agc ctg aca tct gag gac tct gct gtc tat ttc 288
Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95
tgt gca aga ttg cgg aac tgg gac gag gct atg gac tac tgg ggc caa 336
Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln

100	105	110	
ggg acc acg gtc acc gtc tcc tca ggt ggt ggt ggt tct ggc ggc ggc			384
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly			
115	120	125	
ggc tcc ggt ggt ggt ggt tct gag ctc gtg atg aca cag tct cca tcc			432
Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser			
130	135	140	
tcc ctg gct atg tca gta gga cag aag gtc act atg agc tgc aag tcc			480
Ser Leu Ala Met Ser Val Gly Gln Lys Val Thr Met Ser Cys Lys Ser			
145	150	155	160
agt cag agc ctt tta aat agt agc aat caa aag aac tat ttg gcc tgg			528
Ser Gln Ser Leu Leu Asn Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp			
165	170	175	
tac cag cag aaa caa ggg cag cct cct aaa ctg ctt atc tat ggg gca			576
Tyr Gln Gln Lys Gln Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala			
180	185	190	
tcc att aga gaa tct tgg gtc cct gat cga ttc aca gga agt gga tct			624
Ser Ile Arg Glu Ser Trp Val Pro Asp Arg Phe Thr Gly Ser Gly Ser			
195	200	205	
ggg aca gac ttc act ctc acc atc agc agt gtg aag gct gaa gac ctg			672
Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala Glu Asp Leu			
210	215	220	
gca gtt tat tac tgt cag caa tat tat agc tat ccg tac acg ttc gga			720
Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Tyr Thr Phe Gly			
225	230	235	240
ggg ggg acc aag ctt gag atc aaa			744
Gly Gly Thr Lys Leu Glu Ile Lys			
245			

<210> 77
 <211> 248
 <212> PRT
 <213> Mus sp.

<400> 77

Glu Val Gln Leu Leu Glu Gln Ser Gly Ala Glu Leu Val Arg Pro Gly
1 5 10 15

Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ala Phe Thr Asn
20 25 30

Tyr Trp Leu Gly Trp Val Lys Gln Arg Pro Gly His Gly Leu Glu Trp
35 40 45

Val Gly Asp Ile Phe Pro Gly Ser Gly Asn Ala His Tyr Asn Glu Lys
50 55 60

Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Tyr Thr Ala
65 70 75 80

Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
85 90 95

Cys Ala Arg Leu Arg Asn Trp Asp Glu Ala Met Asp Tyr Trp Gly Gln
100 105 110

Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
115 120 125

Gly Ser Gly Gly Gly Gly Ser Glu Leu Val Met Thr Gln Ser Pro Ser
130 135 140

Ser Leu Ala Met Ser Val Gly Gln Lys Val Thr Met Ser Cys Lys Ser
145 150 155 160

Ser Gln Ser Leu Leu Asn Ser Ser Asn Gln Lys Asn Tyr Leu Ala Trp
165 170 175

Tyr Gln Gln Lys Gln Gly Gln Pro Pro Lys Leu Leu Ile Tyr Gly Ala
180 185 190

Ser Ile Arg Glu Ser Trp Val Pro Asp Arg Phe Thr Gly Ser Gly Ser
195 200 205

Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Val Lys Ala Glu Asp Leu
210 215 220

Ala Val Tyr Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Tyr Thr Phe Gly
225 230 235 240

Gly Gly Thr Lys Leu Glu Ile Lys
245